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Result
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Perfect score:
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         score greater
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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           of hits satisfying chosen parameters:
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(without alignments)
4296.941 Million cell updates/sec
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Q92SMU8
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  Q9p2m2 homo sapien
Q8r215 mus musculu
Q86dp2 homo sapien
Q42206 arabidopsis
Q9p2r4 arabidopsis
Q9p2r4 arabidopsis
Q8v7g7 tt virus
Q42584 arabidopsis
Q9smu8 arabidopsis
Q9smu8 arabidopsis
Q9smu8 arabidopsis
Q9sd07 streptococc
Q92114 rickettala
Q92891 Chlamydia p
Q42958 chlamydia p
Q42958 schizosacch
Q95xn6 ceanorhabdi
Q9w2p5 drosophila
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Q8ZQT2
Q8Z8B5
Q8SUY1
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033IV4
5 Q8ZIP0
6 Q8ZIP0
7 Q9VV45
7 Q94LR6
7 Q94D0
7 Q9V00
7 Q92E00
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Q9EU16
005567
Q9HT32
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Q9RAN1
Q94045
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RESULT 1
Q9P2M2
ID Q9P2M2
PRELIMINARY;
AC Q9P2M2;
DT 01-CCT-2000 (TrEMBLrel. 15, C
DT 01-DEC-2001 (TrEMBLrel. 19, L
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Q9CN76
Q95KA0
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Q8ZD48
Q8ZD48
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Q8ZB48
Q9X327
Q9X948
Q9X948
Q9X948
Q9X951
Q9X952
Q9S5109
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Q93IF7
Q8XSW3
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Q91WP3
Q9Y4S3
Q9PC12
Q9P883
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Q9P883
Q9CY58
Q9CY58
Q9CY58
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Q9CSM7
Q64784
Q64784
Q94818
Q95QG7
Q99833
Q982GG1
Q99186
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Q8WUH0
       Last sequence update)
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Q93if7 propionibac
Q93if7 propionibac
Q93wf1 homo sapien
Q95wf1 homo sapien
Q95wf1 homo sapien
Q95wf1 anabaena sp
Q95wf1 anabaena sp
Q98s36 guillardia
Q98s36 guillardia
Q98s37 streptomyce
Q9n948 trypanosoma
Q9n948 trypanosoma
Q9n949 drosophila
Q55109 synechococc
Q9slb9 arabidopsis
Q91wf3 oryza sativ
Q32863 pedinomonas
Q91wf3 ralstonia s
Q91wf3 ralstonia s
Q94wf3 methanococc
Q899s8 listeria mo
Q90ar0 caenorhabdi
Q82s88 arabidopsis
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Q9crr7 mus musculu
Q91wp3 mus musculu
Q91wp3 mus musculri
Q9y483 homo sapien
Q9y483 homo sapien
Q9y612 xylella fas
Q99w60 staphylococ
Q9p883 agarricus bi
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Q64784 avian adeno
Q8xp53 clostridium
Q94818 homo sapien
Q9sqg7 lycopersico
Q9sqg7 lycopersico
Q9sqg8 arabidopsis
Q99xa3 staphylococ
Q8w071 oryza sativ
Q9h1w6 homo sapien
Q8x562 mus musculu
Q93356 emericella
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Q9dby6 mus musculu
Q9bty3 homo sapien
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Q9bum4 homo sapien
Q8wuh0 homo sapien
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O64275 lactococcus
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Q8vhu3 rattus norv
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SEQUENCE
Q8F215;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 32.6 KDa protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:65-73(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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KIAA1324.
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                                                                                                                                                                                                                                                                                                                                                                                                                            554;
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                                                                                                                  EGEDVEDDLIFTSK 554
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                                                                                                                                                       idfwlkvgisagtctailltvltcyfwkknQkleykysklvmnatlkdcdlpaadscaim
                                                                                                                                                                 IDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADSCAIM
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                                                                     PRELIMINARY;
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%; Pred. No. 0;
0; Mismatches
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120 544 60

664 180 604

240

300

540 964 904 420 844 360 784

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Matches 91
                                                                                                       Q42206;
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Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO55902; BAB71041.1;
InterPro; IPRO01881; EGF Ca.
SWART; SM00179; EGF CA; I.
SWART; SM00179; EGF CA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Wishikawa T., Kimura K., Yamashita H., Watsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                           01-NOV-1996
01-DEC-2001
Peroxidase (Fragment).
                                                                                 01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ31340 fis, clone MESAN1000035, weakly similar to major
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                          43 GVAYTSECFPCKPGT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 SKLVMNATLKDCDLPAADSCAIMEGEDVEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WREPKLCSGGISLPEQRVTICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKY 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKLVMNATLKDCDLPAADSCAIMEGEDVEDD 972
                                                                                                                                                                                                                                                                                                                                                                 15;
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. )
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                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 15;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%; Score 91;
100.0%; Pred. No.
                     01,
19,
             Last sequence update)
Last annotation update)
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                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                       97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                 3.5e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3e-92;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 300;
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RESULT 6
Q9C5R4
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Q9PXT8
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                                                                                                                                                                               Query Match
Best Local
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  Q9C5R4;
Q9C5R4;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                        Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                            Higashi Y., Kakumu S., Yoshioka K., Wakita T., Mizokami M., Ohba K., Ito Y., Ishikawa T., Takayanagi M., Nagai Y., "Dynamics of genome change in the EZ/NS1 region of hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
                                                                                                                                                                                                                                                       ProDom; PD186062; HCV_NS1; 1.
                                                                                                                                                                                                                                                               Virology 197:659-668(1993).
InterPro; IPR002531; HCV_NS1.
Pfam; PF01560; HCV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                       132 HGFASLSA 139
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94069940; PubMed=8249288;
                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome polyprotein [Contains: envelope glycoprotein E2/NS1 (GP68)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PXT8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9PXT8
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. COLUMBIA; TISSUE=SEEDLING; Desprez T., Amselem J., Chiapello H., Caboche M., Hofte Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                          n vivo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00436; PEROXIDASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00141; peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z29133; CAA82392.1; -. HSSP; P00433; ZATJ.
                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 VILAGGPS 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 VILAGGPS 89
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                                                                                                                 HGFASLSA 33
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133 AA;
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                                                   PRELIMINARY;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 8; DB 10; Length 97; ilarity 100.0%; Pred. No. 5.2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                            14623 MW; D04D3DC045350488 CRC64;
                                                                                                                                                           100.0%; **
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                                                                                                                                                                           0.8%; Score 8;
100.0%; Pred. No
           Last
                          Created)
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                                                                                                                                                               Mismatches
           sequence update)
                                                                                                                                                                           No.
                                                 248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AA.
                                                                                                                                                                          DB 12; Length 133;
o. 6.8;
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                                                                                                                                                                                                                                                                                                                                                                                                               no DNA stage; Flaviviridae;
                                                                                                                                                              0;
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Last annotation update)

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Best Local S
Matches 8
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Best Local
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Q8V7G7;
01-MAR-2002
01-MAR-2002
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Interpro
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SEQUENCE FROM N.A.
Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
Shinn P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AT3G49120.
AT3G49120/T2J13 40.
Arabdidopsis thaTiana (Mouse-ear cress).
Arabdidopsis thaTiana (Mouse).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
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TT virus.
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PRINTS; PR00458; PEROXIDASE 2;
PROSITE; PS00436; PEROXIDASE 2;
SEQUENCE 248 AA; 27154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Analysis of the complete genomes of thirteen TT virus variants classifiable into the fourth and fifth genetic groups, isolated viremic infants.", Arch. Virol. 147:21-41(2002).

EMBL; AB064603; BAB79340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JT41F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002
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                                                                                                                                                                                                                                                                                                                               EMBL; AB064603; BAB79340.1; -
InterPro; IPR004118; TT_ORF2.
Pfam; PF02957; TT_ORF2; 1.
SEQUENCE 302 AA; 32388 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peng Y.H., Nishizawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2131.
MEDLINE=21344401; PubMed=11855633;
Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 VTLAGGPS 146
    278 DSAAESTG 285
                                                                              145 DSAAESTG 152
                                                                                                                                                         Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTLAGGPS 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ssDNA viruses; unclassified ssDNA viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.: (TrEMBLrel.: (TrEMBLrel.:
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                                                                                                                                                                  Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 8; 
100.0%; Pred. No.
                                                                                                                                                                      0.8%; Score 8; DB : 100.0%; Pred. No. 14 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20,
20,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                    CD492A959881A33C CRC64;
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                                                                                                                                                                                                                                                     12; Length 302;
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                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT 8
PRA REAR E SERVE S
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Best Local (
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Q42584; Q1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9SMU8;
Q9SMU8;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol. 104:285-286(1994).
EMBL; X71794; CAA50677.1; -.
HSSP; P00433; 2ATJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00435; PEROXIDASE_1; 1.
PROSITE; PS00436; PEROXIDASE_2; 1.
Oxidoreductase; Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002016; Peroxidase. Pfam; PF00141; peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intapruk C., Takano M., Shinmyo A.; "Nucleotide sequence of a new cDNA for peroxidase from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
peroxidase (Putative peroxidase protein) (AT3949120/T2J13_40).
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  Submitted [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideursids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T2J13.40.
                         Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu
Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R.,
"Full Length cDNA of gene T2J13.40 (GI.6522554).";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                 Rieger M., Gabel C., Mueller-Auer S., Schaefe
Mewes H.W., Lemcke K., Mayer K.F.X., Quetier I
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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es 8; Conserv
                                                                                                                                                                                            Arabidopsis sequencing project; omitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
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100.0%; Pred. N
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Last annotation updat
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Quetier F., Salanoubat
Bank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 AA.
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                                                                                              P., Lee J.
Theologis
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                                                                                                                           Lee J.
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Q9A0D7
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Best Local :
 STRAIN=SF370 / ATCC 700294 / SEROTYPE M1; MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                               SEQUENCE FROM N.A.
                                                                              Streptococcaceae;
                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                 Streptococcus
                                                                                                                                            Hypothetical protein SPy0818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim C.J., Chen H., Cheuk R., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis ORF clones.", Theologis A., Ecker J.R.; Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     Q9A0D7
                                                                NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                139 VTĽAGGPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00435; PEROXIDASE 1; 1. PROSITE; PS00436; PEROXIDASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Myuyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                  680 VTLAGGPS 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002016; Peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Arabidopsis cDNA clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00141; peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL122967; CAB61998.1;
AF326680; AAG41462.1;
AF339700; AAK00382.1;
AF419569; AAL31901.1;
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P00433; 2ATJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length cDNA of gene T2J13.40 (GI:6522554).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                               353 AA;
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                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                              pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL84990.1; -.
                                                                       Streptococcus.
PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                               38832 MW;
                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 8;
100.0%; Pred. No
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MEDLINE-99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Clinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                              Q9Z891;
Q9Z891;
                                                                     SEQUENCE FROM N.A.
                                                                                                    Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                           Hypothetical protein CPn0458
                                                                                                                                                                    01-MAY-1999
01-MAY-1999
                                                                                            NCBI_TaxID=83558
                                                                                                                                                           01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                      341 PRGDYIAF 348
                                                                                                                                                                                                                                                                                           161 PRGDYIAF 168
                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21442074; PubMed=11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TolB protein. TOLB OR RC0406.
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R., "Complete genome sequence of an M1 strain of Streptococcus pyogenes.", Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                           "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsiaceae; Rickettsieae;
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                                                                                                                                                                                                                                                                                                                    Similarity
8; Conserv
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                   444 AA;
                                                                                                                                                  (TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                            (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                 49080 MW;
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100.0%; Pred. N
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100.0%; Pred. N
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19,
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                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia
                                                                                                                                                                                                                                                                                                                                                                3A0EE0543E53D7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                       695 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 AA.
                                                                                                 Chlamydophila
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RESULT 13
Q9JS58
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042958
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Q9JS58;
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EMBL; AE001630; AAD18600.1; --
Hypothetical protein; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Salzberg S.L.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein CDU0458.
CPJ0458 OR CP0294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shirai M., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
from Japan and CWL029 from USA.";
Mucleic Acids Res. 28:2311-2314 (2000).
EMBL; AE002191; AAF38151.1; -.
EMBL; AP002546; BAA98664.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AR39
                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical 82.9 kDa protein C19G7.10C in chromosome
SPBC19G7.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
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                                                                                                                                                                                                                                                                                                                                    Hypothetical protein
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
              Schizosaccharomyces pombe (Fission yeast)
                                                                                                        042958;
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wes 8; Conserv
                                                                                                                                                                                                                               868 VSSCVAGI 875
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                                                                                                                                                                                                  VSSCVAGI 74
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                                                                                                                                                                                                                                                                                                                     695 AA;
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                                                                                                                          PRELIMINARY;
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100.0%; Pred. No
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446CFFE81014693B CRC64;
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                                                                                                                                                                                                                                                                             No.
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                                                                                                                      744 AA
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RESULT 15
Q95XN6
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Best Local S
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Best Local S
Matches 7
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Q95XN6;
01-DEC-2001 (
01-DEC-2001 (
01-MAR-2002 (
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Y71G12B.14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology. The C
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                       Pfam; PF01423; Sm; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                   "Direct Submission."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AC035726; ARX73913.1; -. InterPro; IPR001163; SNRNP_Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of C. elegans co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "denome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium
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                                                                                                                                                                                                  SEQUENCE
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STRAIN=BRISTOL N2;
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                                              237 RGNNVLY 243
65
  RGNNVLY
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7; Conserva
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                                                                                                                                                                                                  77 AA; 8602 MW;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No
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100.0%; Pred. No. 55
tive 0; Mismatches
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RESULT 16 Q9W2P5 ID Q9W2P5

PRELIMINARY;

PRT;

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                                                                                                                                                                                                                       Matches
O22823;
01-JAN-1998 (TrEMBLrel. 05, Created)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                       Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                               PF01423; Sm;
NCE 79 AA;
                                                                                                                                                                                                                                                                                                                            IPR001163; snRNP_Sm.
                                                                                                                                                                                                                 Conservative 0;
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                     9023 MW; 0480FAC62A4DAF5B CRC64;
                                                                                                                                                                                                             0.7%; Score 7; DB 9
100.0%; Pred. No. 56,
ive 0; Mismatches
                                         91
                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                    Length 79;
                                                                                                                                                                                                               Indels
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RESULT 18
Q9M1Z3
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     Query Match
Best Local Similarity
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                                                                                            SEQUENCE
                                                                                                                                        InterPro; IPR001163; snRNP_Sm.
                                                                                                                                                                       EMBL; AL138647; CAB75800.1;
                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
U6 snENA-associated Sm-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9M1Z3;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9M1Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001163; snRNP_Sm.
Pfam; PF01423; Sm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC002333; AAB64025.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      copennaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 RGNNVLY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:761-768(1999).
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STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative small nuclear ribonucleoprotein polypeptide F.
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les 7; Conserv
                                                                                   PF01423; Sm;
NCE 91 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribonucleoprotein
                                                                                 9913 MW;
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  0.7%;
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  Score 7; Pred. No.
                                                                           950E3FE402F92045 CRC64;
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DB 10;
). 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Embryophyta;
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                                                                                                                                                                                                                                                                                                                                               Mewes H.W.,
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RESULT 19
Q9F1F2
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Q9XJP1
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                                                                                         Query Match
Best Local (
                                                           Matches
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De Boever E.H., Clewell D.B., Fraser C.M.;
"Enterococcus faecalis conjugative plasmid pAM373: complete nucleotide sequence and genetic analyses of sex pheromone response.";
MOI. Microbiol. 37:1327-1341(2000).
EMBL; AB002565; AA040455.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 93 AA; 10366 MW; 344C9A25E2DD1922 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 21, Last annotation update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
proliferating cell nuclear antigen (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                   "Proliferating cell nuclear antigen in the brown tide alga."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF126735; AAD29399.1; -.
HSSP; P12004; 1AXC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XJP1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; stramenopiles;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=PT-1;
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                                                                                                                                                                                          SEQÜENCE
                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                          InterPro; IPR000730; Pr_cel_nuc_antig. Pfam; PF02747; PCNA_C; 1. ProDom; PD002673; Pr_cel_nuc_antig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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   788 ESLGIPD 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TaxID=44056;
                                                           Similarity 7; Conserv
                                                                                                                                                                                          100
100 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                               Conservative
                                                                                                                                                                                          11104 MW; 0579A7DA2EF0C773 CRC64;
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                                                                                             0.7%; Score 7; 1
100.0%; Pred. No.
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100.0%; Pred. No.
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MEDLINE=21357209; PubMed=11463916;

MEDLINE=21357209; PubMed=11463916;

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dodson R.J.,

Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam I.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

"Complete genome sequence of a virulent isolate of Streptococcus

pneumoniae.";

Polician R. (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein SP0650.
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 293:498-506(2001).
EMBL; AE007374; AAK74796.1; -.
TIGR; SP0650; -
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SEQUENCE 106 AA; 12657 MW; 4C32886B5A4B7572 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Possible kiaa0568 protein (Fragment).
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SEQUENCE
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                                                                                                                                         Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AL390935; CAC00863.1; -.
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o. 73;
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                                            DB 5;
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Marchenko G.N., Marchenko N.D., Tsygankov Y.D., Chistos
"Organization of threonine biosynthesis genes from the
methylotroph Methylobacillus flagellatus.";
Microbiology 145:3273-3282(1999).
EMBL; L78665; AAF21127.1; -.
EMBL; L78665; AAF21127.1; -.
EMBL; L78665; AAF21127.1; -.
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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PGSLLLP 43
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01-MAY-1999 (TrEMBLrel. 10, L;
01-MAY-1999 (TrEMBLrel. 10, L;
01-MAY-1999 (TrEMBLrel. 10, L;
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Q1-FEB-1997
01-FEB-1997
01-DEC-2001
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NON_TER 1 1
                                                                                                                                                 Chen Q., Wahlgren M.;
Submitted (DEC-1997)
                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata;
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HSSP; P53999; 1PCF.
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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Enkarvota; Metazoa; Nematoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
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                                                                        Local Similarity les 7; Conserv
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132 AA;
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(TrEMBLiel. 02,
(TrEMBLiel. 19,
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100.0%; Pred. No.
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Caenorhabditis.
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SEQUENCE FROM N.A.

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SETRAINATCC 35092 / DSM 1617 / P2;

X MEDLINE-2132296; PubMed=11427726;

X AMADIENE-2132296; PubMed=11427726;

X She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

X AMAYEZ M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

X AMAYEZ M.J., Chan-Weiher C.C., Coordon P.M.K.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

X Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

X Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

Y The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Y Proc. Natl. Acad. Sci. U.S.A., 98:7835-7840(2001).

X EMBL; AE006899; AAK43178.1;

X EMBL; AE006899; AAK43178.1;

X EMBL; AE006899; AAK43178.1;

X EMBL; AE006899; AAK43178.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21153631; PubMed=11254626;
Haneda T., Okada N., Nakazawa N., Kawakami T., Danbara H.;
"Complete DNA Sequence and Comparative Analysis of the 50-Kilobase
Virulence Plasmid of Salmonella enterica Serovar Choleraesuis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enterica subsp. enterica serovar Choleraesuis.
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EMBL; AB040415; BAB20547.1; -.
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hetical AA; 15459 MW;
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(TremBLrel. 18, Last annotation update)
1 protein SSO3078.
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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E0CAC16D74E039A5 CRC64;
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01-NOV-1998 (TEMBLICAL 08, La
Hypothetical 15.8 kDa protein.
MLCB33.17.
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Submitted (APR-1997)
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                                                                                                                                                             MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
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28 LLLWAGT 34

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RESULT 32
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      Query Match
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                                                                                                                                                                                                                                               Q9GQD9;
Q9GQD9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9U732
O9U732
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 17, Last annotation update)
O1-TUN-2001 (Trembl. 17, Last annotation update)
                                                                                                                                                                                                Cryptosporidium muris.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
                                         NON_TER
                                                                                    "Sequence Differences in the Diagnostic Target Region of the Oocyst Wall Protein Gene of Cryptosporidium, Parasites.";
Appl. Environ. Microbiol. 66:5499-5502(2000).
                                                                                                                                                               STRAIN=34;
                              SEQUENCE
                                                              PROSITE;
                                                                                                                                             Xiao L
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                              NCBI_TaxID=5808;
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MEDLINE-99437830; PubMed=10508071;

Sulaiman I.M., Xiao L., Lal A.A.;

"Evaluation of cryptosporidium parvum genotyping techniques.";

Appl. Environ. Microbiol. 65:4431-4435(1999).
                                                                                                                                                                                                                                                                                                                  600560
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161580; AAF04006.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
Occyst wall protein (Fragment).
Cryptosporidium serpentis.
Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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                                                                                                                                                                                                                                                                                                                                                                         93
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                                                                                                                                                                                                                                                                                                                                                                      CPPNTIL 99
                                                                ., Limor J., Morgan U.M., Sulaiman I.M., Thompson R.C.A.,
                                                   PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002086; Aldehyde_dehydr
                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 AA;
                           163
                                       163
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                           AA;
                         17295 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17221 MW; 5DDAEA8331D52FFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; P
  0.7%; Score 7;
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                      734E427DCFB9D19E CRC64;
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                                                                                                                                                                                                                                                                                                           163 AA.
 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 163;
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Length 163;
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DE Q833X6
AC Q833X6;
AC Q833X6;
AC Q833X6;
AC Q853X6;
DT 01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Disease resistance-like protein 17-36 (Fragment).
OS Mentha longifolia (Horse mint).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiaceae; Mentha.
Q9U733
                         RESULT 35
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Q8S448
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                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                            Davis T.M., Vining K.J., Smith C.A., Zhang Q., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                 EMBL; AF474173; AAL83251.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Disease resistance-like protein 585-6 (Fragment).
Mentha longifolia (Horse mint).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiaceae; Mentha.
                                                                                           787 LESLGIP 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis T.M., Vining K.J., Smith C.A., Zhang Q., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL, AF469686; AAL83215.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8S448
Q8S448;
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                                                                  87 LESLGIP 93
                                                                                                                      Local Similarity nes 7; Conserv
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                                                                                                                                                                           165 AA;
                                                                                                                                                                                           165
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 AA; 18180 MW; 61596CB7937AFDDF CRC64;
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                                                                                                                                                                     18312 MW; 91BB59DD313239C2 CRC64;
                                                                                                                                   100.0%;
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rive 0; Mismatches
                                                                                                                                0.7%; Score 7; 1
100.0%; Pred. No.
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100.0%; Pred. No
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Q9U733

PRELIMINARY;

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167 AA.

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AC DE PRESENTATION OF THE 
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OS Crypt GN OWP.

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00cyst wall protein (Fragment).
Cryptosporidium muris.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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01-MAR-2001
01-MAR-2001
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MEDILINE=99437830; PubMed=10508071;

Sulaiman I.M., Xiao L., Lal A.A.;

Sulaiman I.M., Siao L., Lal A.A.;

"Evaluation of cryptosporidium parvum genotyping techniques.";

Appl. Environ. Microbiol. 65:4431-4435(1999).

EMBL; AF161579; AAF04005.1; -

EMBL; AF161579; AAF04005.1; -
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InterPro; IPR002086; Aldehyde_dehydr.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
Q9GQC8;
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence Differences in the Diagnostic Target Region Wall Protein Gene of Cryptosporidium Parasites."; Appl. Environ. Microbiol. 66:5499-5502(2000). EMBL, AF366262, AAG39043.1; -. InterPro; IPR002086; Aldehyde_dehydr. PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
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Xiao L., Limor J., Morgan U.M., Sulaiman I.M., Thompson R.C.A.,
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167 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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100.0%; Pred. No. 1.1e-
tive 0; Mismatches
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[00.0%; Pred. No. 1.1e+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 167;
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Q9S7Q9
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PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
NON_TER 1 1 1
NON_TER 167 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9S7Q9
Q9S7Q9;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cryptosporidium serpentis.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                   STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0705D01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matesumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Oryza sativa (Rice).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence Differences in the Diagnostic Target Region Wall Protein Gene of Cryptosporidium Parasites.";
hppl. Environ. Microbiol. 66:5499-5502(2000).
MRI; AP266275; AAG39056.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al A.A.
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                                                                                                                                                                                                       Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases EMBL, APO00570; BAA85199.1; -. EMBL, APO00492; BAA84624.1; -. SEQUENCE 173 AA; 19923 MW; 636824223DD0C29D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone:P0711E10."
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                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
131 QSYTYII 137
                                                   535 QSYTYII 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 CPPNTIL 103
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ses 7; Conserv
                                                                                                                              Local
                                                                                                 Similarity 7; Conserv
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                                                                                0.7%; Score 7; ilarity 100.0%; Pred. No. Conservative 0; Min--
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2E6AA3161B4243F7 CRC64;
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                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                    DB 10; 1
b. 1.1e+02
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a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1e+0
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                                                                                                                                                            Length 173;
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                     Query Match
Best Local :
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                                                          SEQUENCE
                                                                     NON_TER
                                                                                     Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF134401; AAD24480.1; -.
                                                                                                                               SEQUENCE TISSUE=TESTIS;
TISSUE=TESTIS;
T.R., Zheng L.,
                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel 12, Created)
01-NOV-1999 (TrEMBLrel 12, Last seq
01-NOV-1999 (TrEMBLrel 12, Last ann
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                        Putative espin (Fragment).
Homo sapiens (Human)
                                                                                                                     Bartles J.R., Zheng L., Li A., Wang M.;
"Organization and chromosomal location of the espin gene in the
                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                     Q9Y329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
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SMART; SM00239; C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 21.0 kDa protein (Fragment)
Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
                                                                                                                                                                                                                                                                                                                                                                                     954 DLPAADS 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptam; PF00168; C2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20223868; PubMed=10759889;
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       Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                              121 DLPAADS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                                    192 AA;
                                                                   192
                                                                                                                                                                                                                                                                                                                                                                                                                                             188 188
188 AA; 21013 MW; 59E63D8C2BED8750 CRC64;
       Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                               21971 MW; 44236A20760AEEF6 CRC64;
  0.7%; Score 7; 1
100.0%; Pred. No.
tive 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    0.7%; Score 7: DB 3; 100.0%; Pred. No. 1.2e-
                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                          Last sequence update)
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                                                                                                                                                                                         Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
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     Mismatches
                                                                                                                                                                                                                                                                                               192 AA.
                         DB 4;
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               1.2e+02;
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                        Length 192;
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01-JAN-1998
01-JUN-2002
                 EMBL; U83136; AAB61906.1;
InterPro; IPR003439; ABC transportr.
Pfam; PF00005; ABC tran; 1.
ProDom; PD000006; ABC transportr; 1.
                                                                                                                         Patterson C.S., Donohue T.J., "Identification and characterization of putative cytochrome maturation genes (ccmABCDG) from Rhodobacter sphaeroides."; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
  TIGRFAMs;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=2.4.1;
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                      Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              033570;
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Pfam; PF01551; Peptidase M37; T.

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.

SEQUENCE 197 AA; 21348 MW; 7E0A29BC0874CC50 CRC64;
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical ABC transporter.
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Q9RWR8;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20036896; PubMed=10567266; Mitte O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Bamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Bamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Nakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001918; AAF10178.1; -. TIGR; DR0598; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 İYTAAGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 IYTAAGA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTVLSGI 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
TIGR01189; ccmA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein DR0598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.7%; Score 7; DB 16; L
100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                         subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 197;
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 음. 성
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel 19, Created)
01-DEC-2001 (TrEMBLrel 19, Last sequence update)
01-DEC-2002 (TrEMBLrel 21, Last annotation update)
01-UN-2002 (TrEMBLrel 51, Last annotation update)
Putative integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                   STRAIN=A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kollins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SC01316 OR SCBAC36F5.27C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q93IV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 PAGTEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 PAGTEPA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saunders D.,
                                                                                                                                                                               coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL592292; CA642863.1; -.
InterPro; IPR000252; DedA.
InterPro; IPR000794; Ketoacyl-synt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                    INTERFACE, ALL INTERFACE SYNTHASE; UNKNOWN 1.
PROSITE; PS00606; B KETOACYL SYNTHASE; UNKNOWN 1.
PROSITE; PS00606; B KETOACYL SYNTHASE; UNKNOWN 1.
PROSITER; PS00606; B KETOACYL SYNTHASE; UNKNOWN 1.
                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                 787
25
   LESLGIP 31
                                   LESLGIP 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00211; ABC TRANSPORTER; UNKNOWN_1.
210 AA; 21817 MW; 72C42BE3B1804D
                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harris
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill J., Barrell B. N-2001) to the EMBL/GenE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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100.0%; Pred. No.
                                                                                     100.0%;
                                                                                     0.7%; Score 7;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrell·B.G., Rajandream M.A.
EMBL/GenBank/DDBJ databases.
                                                                     <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72C42BE3B1804D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                     DB 16; Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 210;
                                                                         0; Indels
                                                                                                       Length 211;
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RESULT 44
Q8ZIP0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8ZIPO, PRELIMINARY; PRT
Q8ZIPO;
01-MAR-2002 (TrEMBLrel. 20, Creat
01-MAR-2002 (TrEMBLrel. 20, Last
01-JUN-2002 (TrEMBLrel. 21, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative phosphoglycerate mutase (EC GPMB OR YP00455.
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brands H.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001345; PG/BPGM_mu
Pfam; PF00300; PGAM; 1.
PROSITE; PS00175; PG_MUTASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21470413; PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VV45;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ414142; CAC89311.1; -.
                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                              CG12255 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VV45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isomerase; Hypothetical SEQUENCE 215 AA; 238
                                                                                                                                                                                                                                                                                                                                                                                            CG12255
                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 RIPEGES 121
                                                                                                                                                                                                                                        STRAIN=BERKELEY;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             722 RIPEGES 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                 TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOVAR ORIENTALIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cal protein; Complete proteome.
23829 MW; B59BC554434E47FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PG/BPGM_mutase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 7; DB 1
k; Pred. No. 1.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 215;
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RESULT 46
Q94LR6
                        Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                       Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L., White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 23.5 kDa protein.
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                      "Oryza sativa chromosome 10 BAC OSJNBb0011A08 genomic sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                              EMBL; AC034258; AAK54290.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0036618; CG12255.
InterPro; IPR000618; Insect cuticle.
Pfam; PF00379; Chitin_bind_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 DANGETO 349
                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00379; Chitin bind \overline{4}; VCE 217 AA; 2\overline{4}162 \text{ MW};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                        Conservative
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                                                                                                                                                      AA;
      0./.,
100.0%; Pr
                                                                                                                                               23534 MW;
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      0.7%; Score 7; DB 1
100.0%; Pred. No. 1.4
ive 0; Mismatches
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100.0%; Pred. No.
                                                                                                                                        02C547E08745A473 CRC64;
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                                      DB 10; Le
o. 1.4e+02;
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                                                                     Length 223;
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Gaps
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A LA RESTRICTOR OF COCCOCATA TO A RESTRICTOR 
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Q9ZK02
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Best Local :
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                                 Praser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Geinn M., Peterson J., van-Vugt F Palmer N., Haft D., Ross P., Stevenson B., "A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9SOD9;
spirochete Borrelia burgdorferi.";
Mol. Microbiol. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       Plasmid cp32-4.
                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                      Outer surface protein F.
                                                                                                                                                                                                                                          NCBI_TaxID=139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding; Microtubules; Complete proteome.
SEQUENCE 223 AA; 25325 MW; E857C9DD8F676D9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., D. Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ive Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  973 LIFTSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001542; AAD06731.1; ...
InterPro; IPR002453; Beta_tubulin.
InterPro; IPR003754; HEM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative uroporphyrinogen-III synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 LIFTSKN 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 TAAGASD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 TAAGASD 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                        Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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o. 1.4e+02;
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Q93S03
ID Q93S0
ID Q93S0
AC Q93S0
DT 01-DE
DT 01-TI
DE Putat
GN SCO626
OC Actii
RC STRA;
RA Seege
RI Subm;
RA SCORN
RA SCORN
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RA RABDLI
RC STRA;
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Query Match
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Matches 7
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                                                                           REGULATORS.
REGULATORS.

REGULATORS.

EMBL; AL591083; CAC37887.1; -.

InterPro; IPR001647; HTH TetR.

Pfam; PF00440; tetR; 1.

DNA-binding; Transcription regulation.

DNA-binding; 724 AA; 24083 MW; B341DBD4
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InterPro; IPR003483; OspEF.
Pfam; PF02471; OspEF; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q93S03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomycetales, Streptomycineae, Streptomycetaceae, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeger K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 DLEGAVK 369
                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                     Hopwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 DLEGAVK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%;
                            0.7%; Score 7;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No. 1.4e+02;
0; Mismatches 0;
     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4C3AD3F10DC9CD11 CRC64;
                                                                                                                B341DBD44A209CB4 CRC64;
        Mismatches
                                                            DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                  1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 224;
                                                         Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
        0,
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ROCCOGREDITA
                                                                                                                                  RESULT
                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                        Matches
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01-JUN-1998
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     042826
042826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pdh1 protein precursor.
PDH1 OR SPCC1235.08C.
                                                                                                   025822;
                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces.
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                  ÉMBL; AL031764;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iha H., Takimoto M., Danjoh I., Fujiyama A.;
"Identification and characterization of a novel trans-membrane protein
gene, pdh1, from Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98162726; PubMed=9501995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 RIWRLLL 186
                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Uroporphyrinogen III COSYNTHASE (HEMD).
                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                 TRANSMEM
NCBI_TaxID=210; [1]
                                                                                                                                                                                                                                                                                                            TRANSMEM
                  Helicobacter
                             Bacteria; Proteobacteria; epsilon subdivision;
                                        Helicobacter pylori (Campylobacter pylori);
                                                                                                                                                                                                                                                                                                                                                                                                  !- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                214 ELFHLES
                                                                                                                                                                                   783 ELFHLES
                                                                                                                                 51
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                                                                                                                                                                                                                                                                                                                                                                                           D88384; BAA24946.1;
                                                                                                                                                                                                       l Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                               Rajandream M.A., Barrell B.G., Murphy L., Harr:
d (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4:393-396 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (TrEMBLrel. 06, 13 (TrEMBLrel. 06, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
                                                                                                                                                                                                         Conservative
                                                                                                               PRELIMINARY;
                                                                                                                                                                                     789
                                                                                                                                                                                                                                                                                                  27
27
42
63
87
                                                                                                                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                                                                                                                                                                    CAA21112.1;
                                                                                                                                                                                                                                                                                                  226
41
62
65
86
97
                                                                                                                                                                                                      0.7%;
100.0%; Pre
                                                                                                                                                                                                                                                  26021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                             Score 7;
                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                    PDH1 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                     Pred.
                                                                                                                 PRT;
                                                                                                                                                                                                                                                    3C71DB50ECB317B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama A.;
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                      No.
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                                                                                                                  226 AA
                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                     1.4e+02;
                                                                          update)
                                                                                                                                                                                                                                Length 226;
                                  Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                             Harris D.;
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RESULT 52
Q9MP30
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C -!- FUNCTION: COMPLON OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

C -- COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

C -!- COPPLED TO ATP SYNTHESIS (BY SIMILARITY).

C -!- COPPLED TO THE GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

C -!- COPPLET TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

C -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

C -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

C -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL; API46718; AAP66718-1; --

REMBL; AF146718; AAP66718-1; --

REMBL; AF146718; AAP66718-1; --

REMBL; AF146718; CYTOCHROME B FAMILY.

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Best Local
                                                                                                                                                                                                                                                                     Chiotis M., Jermin L.S., Crozier R.H.;
"A molecular framework for the phylogeny of the ant subfamily Dolichoderinae.";
                                                                                                                                                                                                                                                                                                                                      STRAIN=ACLP;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopte Formicidae; Dolichoderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome b (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9MP30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO02453; Beta tubulin.
InterPro; IPRO03754; HEM4.
Pfam; PF02602; HEM4; 1.
PROSITE; PS00228; TUBULIN B AUTOREG; 1.
PROSITE; PS00228; TUBULIN B AUTOREG; 1.
GTP-binding; Hypothetical protein; Microtubules; Complete proteome.
SEQUENCE 226 AA; 25862 MW; 82BAF4B54D6AFEBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
EMBL; AE000628; AAD08269.1; -.
TIGR; HP1224; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E. Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forelius chalybaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9MP30;
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=121505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pyiori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=26695 / ATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 973 LIFTSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIFTSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, 17 (TremBLrel. 15, 19, 19, 19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Endopterygota; Hymenoptera; Apocrita; Aculeata; erinae; Forelius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 7; DB 1
100.0%; Pred. No. 1.4
tive 0; Mismatches
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Le
5. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā
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                                                                                                                                                          ARE NOT COVALENTLY
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RESULT 54
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    AGO DITORIA DE LA COMBANA DE L
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                              01-JUL-1997
01-JUL-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBSUT3 PRELIMINARY; PKI; COUNTY; QBSUT3; QBSUT3; QBSUT3; CPSUT3; QBSUT3; Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                    Flavoprotein
                                                                                                                                                                                                                                                                                                  007821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence and gene compaction Encephalitozoon cuniculi.", Nature 414:450-453 (2001).
EMBL, AL590448, CAD26335.1; -.
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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
MEDLINE=95014061; PubMed=7928987;
                          SEQUENCE FROM N.A
STRAIN=GB17;
                                                                                 NCBI_TaxID=266;
                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                              Paracoccus denitrificans
                                                                                                                                                                                                                                                                                                                         007821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein SEQUENCE 246 AA; ;
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Submitted (APR-2001)
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NCBI_TaxID=6035;
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(TrEMBLrel.
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                                                                                                                                                                                                      (Fragment)
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                                                                                                                                 alpha subdivision; Rhodobacter group;
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Last sequence update)
Last annotation update)
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GN L2802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9N9P6;
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Wodara C., Bardischewsky F., Friedrich C.G.;
"Cloning and characterization of sulfite dehydrogenase, two c-type
cytochromes, and a flavoprotein of Paracoccus denitrificans GB17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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NCBI_TaxID=5664;
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HSSP; Q06530; 1FCD.
NON_TER 247 247
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Wodara C., Bardischewsky F., Friedrich
                   SEQUENCE FROM N.A. STRAIN=FRIEDLIN;
                                                                                                                    Ivens A.C., Lewis Smith D.F.;
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Barrell B.G.;
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Volckaert
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(JUN-1997)
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8:135-145(1998)
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S.M., Bagherzad
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A.C.,
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Rajandream M.A.,
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Matches 7
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Q8ZXA9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell B.G.,
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; AL359774; CAB95238.2; -.
EMBL; AL359683; CAC37117.1; -.
"Genome sequence of the hyperthermophilic crenarchaeon aerophilum.", Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002). EMBL; AE009818; AAL63440.1; -. InterPro; IPR003794; DUF191.
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NON_TER
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penici
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2000) to the EM EMBL; AF284064; AAG22769.1; -. EMBL; AF284064; AAG22769.1; -. InterPro; IPR002921; Lipage 3. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X.-F.;
"Cloning and expression of Penicillium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Lin L., Xie B.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                    SEQUENCE FROM:N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
                                                                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoprotei; Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=27334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipase
                                                                                                                           Fitz-Gibbon S.T., Ladner H., Kim U.-J.,
                                                                                                                                                 PubMed=11792869;
                                                                                                                                                                                                                             NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                Pyrobaculum aerophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 PYGSYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 NRGNNVL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01764; Lipase_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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100.0%; Pre
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Last annotation updat
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EMBL/GenBank/DDBJ da
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Pred. No
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), 1.6e+02;
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1.5e+02;
                                                                                                                                                                                                                                                                          Thermoproteales;
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                                                                                                                               Stetter
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                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  존
                                                                                                                               Simon
                                                                                      Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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RESULT 58
Q8STF1
ID Q8STF
AC Q8STF
O1-JU
DT 01-JU
DT 01-J
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Q92TZ9
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Matches
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Best Local
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                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative modification methylase protein.
HEMK2 OR RB1344 OR SMB21514.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizob Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                         Q92TZ9
Q92TZ9;
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL590450; CAD25919.1; -. EMBL; AL590445; CAD26684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence and gene compaction Encephalitozoon cuniculi.";
Nature 414:450-453(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
Submitted (APR-2001) to the EMBL/Genfank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECUI1_0090 (Hypothetical protein
ECU05_1640).
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STRAIN=GB-M1;
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Hypothetical protein; Complete proteome.
SEQUENCE 267 AA; 29602 MW; 08362C2A1FE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon NCBI_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Encephalitozoon cuniculi.
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Pfam; PF02642; DUF191; 1.
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268 AA; 3
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29602 MW; 08362C2A1FE0C293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30530 MW; 4BA693E33A4567D8 CRC64;
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100.0%; Pred. No.
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0; Mismatches
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NO. 1.6e+02;
0;
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o. 1.6e+02;
                                                                                                                                                                                                                                                                                                               A
                                                                Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 268;
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RESULT 61
Q8U7C6
ID Q8U7C
AG Q8U7C
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT ABC t
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Q8YSU3
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Best Local
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Q8U7C6 PRELIMINARY; PKT; 254 AM.
Q8U7C6;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8YSU3;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sas.
Watanabe A., Iriguchi M., Ishikawa A., Kawashima i
Kishida Y., Kohara M., Matsumoto M., Matsuno A., N
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M.,
"Complete carronica ---
                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyanobacterium Anabaena sp. DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Finan T.M., Weidner S., Wong K., Buh:
Vorhoelter F.J., Hernandez-Lucas I.,
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP003591; BAB74688.1; -.
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EMBL; AL603646; CAC49744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete sequence of the 1,683-kb pSymB megaplasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=1021
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                                                                                                                                                                                                                                                                    752 KAGVSSQ 758
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                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 l protein; Complete proteome.
282 AA; 31531 MW; 7EBC9ADCD7A119AE CRC64;
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2 (TrEMBLrel. 20, Lau
2 (TrEMBLrel. 20, Lau
al protein All2989.
                                                                                                                                                                                                                                                                                                                Conservative
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Last annotation update)
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, Buhrmester J., (
Becker A.,
                                                                                                                                                                                                                                                                                                    DB 16; LC., NO. 1.7e+02; 0;
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Kimura T.,
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spanning protein.

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RESULT 62
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Best I
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                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 17, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Alkaline lipase (EC 3.1.1.3) (Triacylglycerol lipase precursor).
Penicillium cyclopium, and
Penicillium expansum.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9P451;
Q9P451;
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Complete proteome.
SEQUENCE 284 AA; 30723 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2322-2328(2001). Science 294:2323-2328(2001). BENBL; ABO09380; ABA45317.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Willin L. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
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Agrobacterium tumefaciens
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
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MEDLINE=21608550; PubMed=11743193;
MEDLINE=21608550; PubMed=11743193;
                 SEQUENCE FROM N.A.
SPECIES-P.expansum; STRAIN-WMC20718;
SPECIES-P.expansum; STRAIN-WMC20718;
Wu M., Qian Z., Win T., Sun C., Huang W.;
Wu M., Qian Z., Tomponing of alkaline lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21608551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. SPECIES=P.cyclopium; Wu M., Qian Z., Min J
                                                                                                                                                                       Submitted
                                                                                                                                                                                "Cloning and sequencing of alkaline cyclopium PG37.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
and sequencing WMC20718.";
                                                                                                                                                                 (JUN-2000) to the
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                                                                                                                                                                                                                                                                                                                                                                    27334;
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                                                                                                                                                                                                                                                                              STRAIN=PG37;
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Pred. No.
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                                                                                                                                                                                                                      Huang W.;
line lipase cDNA from Penicillium
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o. 1.7e+02;
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Rhizobiaceae group;
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                             Penicillium
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Dolan M.,
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Best Local S
Matches 7
           Query Match
Best Local
    Matches
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Q94295;
                                                                                                                                                                                                                                                                                                                                             Hypothetical
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SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF288685; AAF99329.1; EMBL; AF330635; AAK07480.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequencing of triacylglycerol expansum PF898.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. SPECIES=P.expansum; Lin L., Xie B.F., S.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiu S.G
                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; U70858; AAB09178.1; -
InterPro; IPR000276; GPCR Rhodpsn.
INTERPOSE PS50562; G PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                              "The
                                                                                                                                                                       STRAIN-BRISTOL N2;
Graves T., Wohldmann
                                                                                                                                                                                                               Science
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002921; Lipase_3.
                                         Hypothetical SEQUENCE 2:
                                                                                                                                                                                                                                             None;
                                                                                                             Waterston
                                                                                                                        SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                              "Genome sequence of the nematode C. investigating biology. The C. elegascience 282:2012-2018(1998).
                                                                                                                                                                                                                                                     STRAIN=BRISTOL N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 NRGNNVI
                                                                                                   Direct Submission.";
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                                                                                                                                                     sequence of C.
itted (OCT-1996)
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  Similarity 7; Conserv
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                                         al protein.
294 AA; 3
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(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
   0.7%; S ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                             34.3 kDa protein.
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Shi Q.Q., Lin C
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to the
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                                                                                                                                                     cosmid T01C4.";
EMBL/GenBank/DDBJ databases.
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Pred. No.
             Score 7;
Pred. No.
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TRIACYLGLYCEROL LIPASE.
                                                                                                                                                                                                                        ode C. elegans: a platform elegans Sequencing Consort
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                          37760F176CC82405 CRC64;
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Q9AB93
ID Q9AB
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 Wu K., Chung L., Revill W.P., Katz L., Reeves C.D., "The FK520 gene cluster of streptomyces hygroscopicus var. ascomyceticus (ATCC 14891) contains genes for biosynthesis of unusual
                                                                                                                Streptomyces hygroscopicus var. ascomyceticus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                        MEDLINE=20323220; PubMed=10863099;
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                            01-OCT-2000
                                                                                                                                                                                                                                           Q9KIF0;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-1- SIMILARITY: TO OTHER ALPHA SUBUNITS OF SUCCINYL-COA SYNTHETASE, OI MALATE-COA LIGASE AND TO ATP CITRATE-LYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003781; CoA binding.
InterPro; IPR00303; CoA ligase.
Pfam; PF02629; CoA binding; 1.
Pfam; PF00549; ligase-CoA; 1.
                                                                                                             NCBI_TaxID=132248;
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PROSITE; PS01216; SUCCINYL COA LIG 1; 1.
ATP-binding; Ligase; Phosphorylation; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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TIGR; CC0338; -.
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STRAIN=ATCC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AB93;
                                                                                                                                                                                                                                                                                                                                                         181 DPVKGTE 187
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UN-2001 (TrEMBLrel. 17, Last sequence update)
UN-2002 (TrEMBLrel. 21, Last annotation updat
inyl-CoA synthetase, alpha subunit.
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extender units.";
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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100.0%; Pred. No. 1.0
ive 0; Mismatches
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Q98EC8
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Best Local
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InterPro; IPR003781; CoA binding.
InterPro; IPR003781; CoA_Ligase.
Pfam; PF02629; CoA_binding; 1.
Pfam; PF02629; CoA_binding; 1.
Pfam; PF00549; ligase-CoA; 1.
TIGREAM9; TIGR01019; succoAalpha; 1.
PROSITE; PS01216; SUCCINYL_COA_LIG_1; 1.
PROSITE; PS00399; SUCCINYL_COA_LIG_2; 1.
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Best Local !
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     01-MAR-2002
01-MAR-2002
01-JUN-2002
                                             Q8ZLB0;
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                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamot Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last seque
01-UNN-2002 (TrEMBLrel. 21, Last annot
Succinyl-CoA synthetase alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                              Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
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InterPro; IPRO05119; LysR subst.
Pfam; PF03166; LysR substrate; 1.
Pfam; PF03466; LysR substrate; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH LYSR FAMILY; UNKNOWN 1.
DNA-Binding; Transcription regulation.
SEQUENCE 297 AA; 32462 MW; D015FBD4AC59A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MAFF303099;
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                                                                                                                        187 DPVKGTE 193
                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS. EMBL, AF235504; AAF86383.1; -.
                                                                                                                                                 84 DPVKGTE
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o. 1.8e+02;
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STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; PubMed-11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CO-92 / BIOVAR ORIENTALIS;
MEDDINE=21470413; PubMed=11586360;
MEDDINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague."
Nature 413:523-527(2001).
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DPPC OR YPO4001.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-MAR-2002
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Pfam; PF00528; BPD_transp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00528; BPD_transp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ414160; CAC93461.1; -.
InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275
    275
                                                                                920 AILLTVL 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE008868; AAL22489.1; -.
    AILLTVL
                                                                                                                                                            Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                           proteome
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                                                                                                                                                                                                                                                                                                                             300 AA;
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (membrane), dipeptide transport protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32233 MW;
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                                                                                                                                                                                                                                                                                                                             32307 MW;
                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                       0.7%; Score 7; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 1; Pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                             F9F7F4C856E8EB13 CRC64;
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                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8e+02;
                                                                                                                                                                                                       1.8e+02;
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                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                                             Length 300;
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RESULT 69
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Best Local
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MEDINE-21534947; PubMed=11677608;
MEDINE-21534947; PubMed=11677608;
MEDINE-21534947; PubMed=11677608;
Darker C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Siamonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.,
Whitehead S., Barrell B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBZ298;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                       MEDLINE=21608550; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Gordon S., Yoo H., Tao J., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8Z298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:848-852(2001).
EMBL; AL627281; CAD07995.1; -
InterPro; IPR000515; BPD_transp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBUGE1;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SUCCINY1-COA synthetase alpha chain.
SUCCINY1-COA synthetase alpha chain.
SUCCINY1-COA Synthetase (4779.
SUCD OR AUTU2637 OR AGR C 4779.
Agrobacterium tumefaciens (attain C58 / ATCC 33970)
Agrobacterium tumefaciens (attain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8UC61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00528; BPD_transp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision;
Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920 AILLTVL 926
                                                  The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
7; Conserv
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score 7; DB;
; Pred. No. 1.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5087934A5A0857EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobiaceae group;
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                                                                                                                          Dolan M.,
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A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
A Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
B EMBL, AL591792; CA47633.1; --
DR Interpro, IPR003781; COA binding.
Interpro, IPR003781; COA binding.
B Fine: PF02629; COA binding; 1.
DR Ffam; PF02629; COA binding; 1.
DR Ffam; PF02629; COA binding; 1.
DR Pfam; PF02629; COA binding; 1.
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                                                                                                                                                                       Query Match
Best Local
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STRAIN=1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable succinyl-CoA synthetase alpha chain protein
187 DPVKGTE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUCD OR R03054 OR SMC02481.
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q92LJ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 6.2.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE009211; AAL43618.1; -. EMBL; AE008177; AAK88358.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-238(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                          84 DPVKGTE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 DPVKGTE
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                                                                                                                                                                                                                                                           Complete proteome.
E 300 AA; 30927 MW;
                                                                                                                                                                Similarity
                                                                                                                                   Conservative
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                                                                                                                                                                100.0%;
                                                                                                                                                            0.7%; Score 7;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                           FB83DA1106424C20 CRC64;
                                                                                                                            Mismatches
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                                                                                                                                                                                  DB 16; Length 300;
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                                                                                                                                                     1.8e+02;
                                                                                                                        0; Indels
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RESULT 72

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RESULT
Q9Z799
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Q9Z799;
Nucleic Acids Res. 28:2311-2314(2000).
             Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T., "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
                                                                                                                                                      Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
01-UNI-2001 (TrEMBLrel. 17, Last ann
CT580 hypothetical protein.
CPN0807 OR CPJ0807.
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Q8YJE5,
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                           MEDLINE=20330349; PubMed=10871362;
                                                                                                   STRAIN=J138;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE009456; AAL51321.1; -. InterPro; IPR003781; CoA_binding. InterPro; IPR003781; CoA_ligase. InterPro; IPR00303; CoA_ligase. Pfam; PF02529; CoA_binding; 1. Pfam; PF00549; ligase-CoA; 1. Pfam; PF00549; ligase-CoA; 1. PGROSITE; PS01216; SUCCINYL_COA_LIG_1; 1. PROSITE; PS00399; SUCCINYL_COA_LIG_2; UNKNOWN_1.
                                                                                                                                                                                                           MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=83558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";

Broc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAILNE=20020109; PubMed=11756688;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G. Kapatral V. Redkar R.J., Patra G., Mujer C., Los
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 DPVKGTE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 7; Conserv
                                                                                                                                             Genet. 21:385-389(1999).
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E 300 AA; 31234
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arive 0; Mismatches
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100.0%; Pred. No.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        303 AA.
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o. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 300;
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RESULT 74
Q9K1S9
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Best Local (
                                                                                                                                                                                                                                                                                Q56567;
Q56567;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Vibrio anguillarum virC.
Vibrio anguillarum (Listonella anguillarum).
Vibrio anguillarum (Signama subdivision; Vibrio
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.
Eisen J., Fraser C.M.;
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TIGR; CP1064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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MEDLINE=96060845; PubMed=7590330;
Milton D.L., Norqvist A., Wolf-Watz H.;
"Sequence of a novel virulence-mediating gene, virC, anguillarum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000620; DUF6.
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                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=55601;
                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella.
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AP002548; BAA99015.1;
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100.0%; Pred. No.
tive 0; Mismatci
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). 1.8e+02;
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Best Local
STRAIN-GC-92 / BIOVAR ORIENTALIS;

C STRAIN-GC-92 / BIOVAR ORIENTALIS;

X MEDLINE-21470413; PubMed=11586360;

A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

A Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L.,

A Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,

A Peltyell S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Chillingworth T., Cronin A., Davies R.M., Davis P.,

Chillingworth T., Cronin A., Jagels K., Karlyshev A.V.,

A Peltyell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K.,

X Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

X "Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:523-527(2001).

Nature 413:523-527(2001).

Nature 413:523-527(2001).

R EMBL; AJ414143; CAC699485.1; -.

R InterPro; IPR003662; sub_transporter.
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Best Local
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Q8ZI80;
01-MAR-2002
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EMBL; U17054; AAA86984.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spiridonov N.A., Wong L., Johnson G.R.; "Homo sapiens CGI-55 protein mRNA."; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96SB2;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Mammalia; Eutheria;
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01-JUN-2002
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                               TaxID=632;
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                                                                                                                                                                                                                                                                                            Proteobacteria;
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Primates;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FBC15A2A76184429 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     310 AA.
                                                                                 the causative agent of plague.";
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5. 1.9e+02
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RESULT 78
Q9EWZ9
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Best Local
                                                                                                                                                                                       Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                          InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                        Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                   Oxidoreductase
                          PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                                                       EMBL; AL445503; CAC13079.1; -. HSSP; P14061; 1FDU.
                                                                                                                                                                                                                                                                                                              STRAIN=A3(2) / M145;
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Submitted (OCT-2000) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
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01-MAR-2001 (TrEMBLrel 16,
01-JUN-2002 (TrEMBLrel 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00126; HTH 1; 1.
Pfam; PF03466; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
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                                                                                                                  (SDR) FAMILY.
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e EMBL/GenBank/DDBJ databases.
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; Pred. No.
C8AC48B96C0E5B73 CRC64;
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DB 16; I
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                                                                                                                                                                                                                                                                                                                                                                             physical map
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RESULT 80
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Best Local Similarity
Matches 7; Conserva
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Best Local
          "Complete genome structure of the nitrogen-fixing Mesorhizobium loti."; DNA Res. 7:331-338(2000).
                                                 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S., Yamada M., Tabata S.,
                                                                                                                     STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q97FU1;
Q97FU1;
01-OCT-2001
01-OCT-2001
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                       Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                    Permease protein
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                                                                                                                                                                                                                                                                                                             Q98IS2;
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                                                                                                                                                                               NCBI_TaxID=381;
                                                                                                                                                                                           Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 183:4823-4838(2001).

EMBL; AE007761; AAK80582.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 315 AA; 36592 MW; 1188CD3EE3A22124 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M., Bennett G.N., Koonin E.V., Smith D.R., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium acetobutylicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                              306 KIYSINV
                                                                                                                                                                                                                                                                                                                                                                                                                        571 KIYSINV 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 AGEFLOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 AGEFLDM 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
AP002999; BAB49444.1; -.
                                                                                                                                                                                                                                          (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
Dtein of oligopeptide ABC transporter.
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 18, (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein CAC2635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
                                                                                                                                                                                                                                                                                                                        317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Le
b. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Le
o. 1.9e+02;
                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 312;
                                      symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P., Daly M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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RESULT 81
Q43055
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 82
Q91E43
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  RRRR OCCOG DE DITIO
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                              Q91E43;
Q91E43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Populus kitakamiensis (Aspen).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside

eurosids I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
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Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Peroxidase.
Oxidoreductase; Peroxidase.
SEMITENCE 318 AA; 34172 MW; 14838148CD6076E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002016; Peroxidase.
Pfam; PF00141; peroxidase; 1.
PRINTS; PR00458; PEROXIDASE.
PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00436; PEROXIDASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D11102; BAA01877.1; -. HSSP; P00433; 2ATJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence for the genomic DNA encoding an anionic peroxidase gene from a hybrid poplar, Populus kitakamiensis."; Biosci. Biotechnol. Biochem. 57:131-133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=93169019; PubMed=7764045; Kawai S., Matsumoto Y., Kajita S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peroxidase (EC 1.11.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q43055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q43055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai S., Matsumoto Y., Kajita
Morohoshi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3698;
                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seg
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 SLADRLI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   761 SLADRLI 767
Martina B., Osterhaus A.D.M.E., Harder T.C.;
                           STRAIN=PB84;
                                                   SEQUENCE FROM N.A.
                                                                                              NCBI_TaxID=47418;
                                                                                                                              Alphaherpesvirinae; Varicellovirus
                                                                                                                                                         Viruses; dsDNA viruses,
                                                                                                                                                                                                                                  Us2 homologue (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680 VTLAGGP 686
                                                                                                                                                                               Phocid herpesvirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 VTLAGGP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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7; Conserv
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317 AA;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 7; DB 1 100.0%; Pred. No. 1.9 tive 0; Mismatches
                                                                                                                                                         ដូ
                                                                                                                                                       RNA stage; Herpesviridae
                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747A2DDE9C61AEC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K.,
                                                                                                                                                                                                                                                                                                                                                                 325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Le
o. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Loo, 1.9e+02;
                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Katayama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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SOFFI
                                                             RESULT
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                                                                                                                                                                            RX MEDULINE=21016/Z01; FUDDMed=11130/13;
RX Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Ra Balanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Ra Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Ra De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Ra Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Ra Wincker M., Mener G., Lordind R., Brandt P., Nyakatura G.,
Ra Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ra Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Ra Reichelt J., Scharfe M., Schoen O., Bargues M., Duchemin D.,
Ra Rooner R., Laudie M., Berger Llauro C., Purnelle B., Mesuy D.,
Ra Mannhaupt G., Haase D., Schoeff H., Rudd S., Zaccaria P., Mewes H.-W.,
Ra Mannhaupt G., Haase D., Schoeff H., Rudd S., Zaccaria P., Mewes H.-W.,
Ra Rooney T., Rizzo M., Walts A., Utterback T., Vitale D.,
Ra Rooney T., Rizzo M., Walts A., Utterback T., Van Aken S.,
Ra Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
Ra Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
Ra Parser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C.,
Ra Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Ra Parser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C.,
Ra Rasamoto S., Kimura T., Ideaswa K., Kawashima K., Kishida Y.,
Sequence and analysis of chromosome 3 of the plant Arabidopsis
Thallon L. J., Jane J., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9CAX9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification and analysis of immunogenicity of the glycoprotein D equivalentwithin the unique short segment of phocid herpesvirus-1."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJZ09055; CCG1462.1; -
Interpro; IPR003485; US2_Unk.

Pfam; PF02476; US2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e

germatophyta; Magnoliophyta; eudicotyledons; core e

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical 37.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   887 LCSGGIS 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                           EMBL; AC008153; AAG51446.1;
                                                                                   Hypothetical
                                                                                                                                                               Nature 408:820-822(2000)
                                                                                                                            [nterPro; IPR005299; Methytransf_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCSGGIS 293
                                                                                                      PF03492; Methytransf_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
7; Conserv
                                                        protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 7; DB 1
100.0%; Pred. No. 1.9
tive 0; Mismatches
                                                                 37575 MW;
    0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
  Score 7; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2EF22B8FB483D1B9 CRC64;
                                                                   8B3FD25A11B8D700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Lo
                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
        2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 325;
                        Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 84
Q9PQG1
ID Q9PQG
       ACCOUNT OF THE PROPERTY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q97KX8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                             STRAINATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-2135935; PubMcd=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.:
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 18;4823-4838 (2001).
EMBL; AE007594; AAK78764.1; -.
                                                                      InterPro; IPR000522; FecCD.
Pfam; PF01032; FecCD; 1.
ProDom; PD001557; FecCD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                       Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01~JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 407:757-762(2000).
EMBL; AE002110; AAF30739.1; -.
Hypothetical protein; Complete
SEQUENCE 327 AA; 38114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20500219; PubMed=11048724; Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SEROVAR 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ureaplasma parvum (Ureaplasma urealyticum biotype 1)
Bacteria, Firmicutes, Bacillus/Clostridium group, Mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 FMILTLY 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FMILTLV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) (TrEMBLrel. 15, () (TrEMBLrel. 20, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263
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   36552 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              permease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۰,
1BC0BC10C47B0F34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321275386DAF61B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 16; Lu., No. 2e+02; 0;
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                                                                                                                                                                                                                                                                                                                                                                  Soucaille P., Daly M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 327;
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RESULT 87
Q8ZQT2
           DR RET DR REAL REPORTS OF THE PROPERTY OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sancotation update)
3-deoxy-D-arabinoheptulosonate-7-phosphate synthase
phenylalanine repressible) (EC 4.1.2.15).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8RVP3
Q8RVP3;
EMBL; AB008731; AAL19699.1; -.
InterPro; IPR001785; DAHP synth 1.
Pfam; PF00793; DAHP synth 1; 1.
ProDom; PD005060; DAHP_synth1; 1.
                                                                                                                                                                                        McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Li Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvan Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8ZQT2;
                                                                                                                                                                                                                                                                                                                              STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF488305; AAL92037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delannoy E., Patil M., Essenberg M., Jalloul A., Marmey P., Daniel J.-F., Geiger J.-P., Nicole M.; "Gossypium hirsutum bacterial-induced peroxidase (podSSH1).";
                                                                                                              Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AROG OR STM076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peroxidase; Oxidoreductase.
SECUENCE 347 AA; 37407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             יג־יטעא־בעעב (וובאשטרפן. 12, Last annotation update)
Bacterial-induced peroxidase (EC 1.11.1.7).
DONOCCU
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                    "Complete genome sequence of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. REBA B50; TISSUE=2 WEEK OLD COTYLEDONS; Delannoy E., Patil M., Essenberg M., Jalloul A., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PODSSH1
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
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o. 2e+02;
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                                                                                                                                                                                                                                         ., Latreille P.,
ou S., Layman D.,
Mulvaney E.,
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ACOCCO CONTRACTOR CONT
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"her 7; Conserv
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Lyase; Comple
SEQUENCE 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Krogh A., Lareen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Whitehead S., Barrell B.G.; Whitehead S., Barrell B.G.; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Phospho-2-dehydro-3-deoxyheptonate aldolase (DAHP s)
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STY0801.
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Pfam; PF00793; DAHP synth1; 1.
ProDom; PD005060; DAHP synth1; 1.
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SEQUENCE FROM N.A.
                                    NCBI_TaxID=6035;
                                                                                                                                        01-UN-2002 (TrEMBLrel 21, Created)
01-UN-2002 (TrEMBLrel 21, Last sequence up
01-UN-2002 (TrEMBLrel 21, Last annotation
Hypothetical protein ECU07_1170.
                                                                                                                                                                                                                                                                         TAMS8Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi.
                                                                      Eukaryota; Microsporidia;
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                                                                                                 Encephalitozoon cuniculi.
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                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37868 MW; C764207BBAB65FB7 CRC64;
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o. 2.1e+02;
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SO DE RELACIONES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE REAL SERVICES OF SERVIC
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Best Local
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                                                             Q9CN76;
Q9CN76;
01-JUN-2001
01-JUN-2001
01-JUN-2002
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Q92HR6;
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to microcin C7 self-immunity protein.
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Nature 414:450-453(2001).
EMBL; AL590447; CAD25650.1; -.
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Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:2093-2098(2001).
EMBL; AE008629; AAL03243.1; -.
InterPro; IPR003507; UPF0094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=MALISH 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similar to microcin MCCF2 OR RC0705.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia conorii.
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AROG OR PM0563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 NTPTRTF 669
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                                                                (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 21,
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o. 2.1e+02;
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RESULT 92
Q95KA0
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 39.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21145866; PubMed=11248100;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., K
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AB006092; AAK02647.1; -.
                                                                                                                                                                                                                                                EMBL; AB063042; BAB60776.1; -. InterPro; IPR000873; AMP-bind. Pfam; PF00501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                          TISSUE-MEDULLA OBLOGATA;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001785; DAHP_synth1.
Pfam; PF00793; DAHP_synth1; 1.
ProDom; PD005060; DAHP_synth1; 1.
                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 364 AA; 3
                                                                                                                                                                                                                                                                               libraries.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
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             01-MAR-2001
01-JUN-2002
                                                              Q9FCI6
                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
  Putative
                                     01-MAR-2001
                                                  Q9FCI6;
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                                                                                                                                                  412 PAGTEPA 418
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                                                                                                                                                                                       Local
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          1 (TrEMBLrel. 16, 11 (TrEMBLrel. 16, 16, 17) (TrEMBLrel. 21, 21, 17)
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                                                             PRELIMINARY;
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protein
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           Last sequence update)
Last annotation update)
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Mismatches
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o. 2.1e+02;
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o. 2.1e+02;
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                                                                                                                                                                                                Length 364;
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Best Local
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P91984;
01-MAY-1997 (TrEMBLrel. 03, C
01-MAY-1997 (TrEMBLrel. 03, L
01-MAR-2002 (TrEMBLrel. 20, L
C50B6.10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M. Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S. Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seager K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL390968; CAC01332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Cerdeno A.M., Parkhill J.,
                                                                                                                                                                                                                                                                                    C50B6.10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                             SEQUENCE FROM N.A.
                                                                             Submitted (OCT-1996)
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2)
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                                                                                                                                                                              NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGISAGT
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SM00228; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38181 MW; 8900C095D03C17B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%;
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the EMBL/GenBank/DDBJ databases.
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                                                                             the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           371
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                                                                                                                                                                                                                                 Rhabditida; Rhabditoidea;
                                                                             databases
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Best Local S
Matches 7
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EMBL; Z81050; CAB02859.1; -.
InterPro; IPR003002; 7TM_nematode.
InterPro; IPR000168; 7TM_nematode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21, PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

What R., Basham D., Brown D., Chillingworth T., Connor R.,

Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,

Bavies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGR00518; alaDH; 1.

PROSITE; PS00836; ALADH PNT 1; 1.

PROSITE; PS00837; ALADH PNT 2; 1.

PAD; Flavoprotein; Oxidoreductase; Complete proteome.

PAD; Flavoprotein; 38845 MW; 35425DE604EF8199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             none;
"Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL583922; CAC:
HSSP; Q60164; 1HZZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-alanine dehydrogenase ALD OR ML1532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9CBV6;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9СВV6
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Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00368; FADPNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004002; AlaDh_PNT:
InterPro; IPR001327; FAD_Dyr_redox.
InterPro; IPR000205; NAD_binding.
Pfem; PF01262; AlaDh_PNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: FAD (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ieproma; ML1532;
                                                                                                                                                      224 DLEGAVK 230
                                                                                                                                                                                                                    363 DLEGAVK 369
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NCE 371 AA; 42
                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                             Conservative
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(TrEMBLrel. 17, Last seq
(TrEMBLrel. 21, Last ann
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                                                                                                                                                                                                                                                                                                                                                               0.7%;
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annotation update)
                                                                                                                                                                                                                                                                           DB 16; INC. 2.2e+02; 0;
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                                                                                                                                                                                                                                                                                                                                                        Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Q9CRR7;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                Q91WP3 PRELIMINARY; PRT; 386 AA.
Q91WP3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00523; DWA; 1
SMART; SM00524; DWB; 1
NON_TER 377 377
                                SEQUENCE FROM N.A.
TISSUE=SALIVARY GI
                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                  Similar to RIKEN cDNA 1200009K13 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03165; MH1; 1. Pfam; PF03166; MH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q92940; 1MHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK018077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 FHSVELN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          łayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MADH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:1328787; Madh5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHSVELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001132; Dwarfin.
IPR003619; Dwarfin_A.
IPR004863; MH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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(Trembirel. 17, Last seque)
(Trembirel. 21, Last annot;
5 (Drosophila) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAB31063.1;
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Rodentia;
                                                                                                                                                                            Rodentia;
                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42204 MW; 830E5E1452D025DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 7; DB:
100.0%; Pred. No. 2.:
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                        Sciurognathi;
                                                                                                                                                                                                                Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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Storch K.-F.,

H 4

DB 11; Loo. 2.2e+02;

Length 377;

0; Gaps

<u>.</u>

Muridae;

Euteleostomi; Murinae;

update)

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RESULT 99
Q9Y4S3
ID Q9Y4S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         069648
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                                                                                                                                         Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Hornesby T., Jagels K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               069648;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       069648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                       Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Belchi w. Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative anion transporting ATP RV3680 OR MTV025.028 OR MT3782.
                                                                                                                                                                                                                                  TubercuList; Rv3680; -...
InterPro; IPR003348; ArsA_ATPase.
Pfam; PF02374; ArsA_ATPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; NCBI TaxID=1773;
   Q9Y4S3
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                            "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 ADTENKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 ADTENKE 493
                                                                                                                                                                                                                       [ypothetical
                                                                               178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                           24 RLWRLLL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC013665; AAH13665.1;
                                                                             RLWRLLL 184
                                                                                                                                                                                                                                                                                                 AL022121; CAA18002.1;
AE007175; AAK48149.1;
                                                                                                                                         Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 AA;
                                                                                                                                                                                                     386 AA; 41404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                      protein; Complete proteome.
36 AA; 41404 MW; AB6D2D31A44620B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSHKOSH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13665:1; -.
42235 MW; A22FB50BE68F72CB CRC64;
                                                                                                                                    100.0%; +1
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100.0%; Pred. N
                                                                                                                                                        Score 7;
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                                                                                                                                         mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                    DB 16; L., 40. 2.3e+02; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386
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o. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                                                                                                                                                        Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein MT3782)
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Dordin S., Bove J.M., Briones M.R.S.,
Barros M.H., Bonaccorei E.D., Bordin S., Bove J.M., Briones M.R.S.,
Al Bueno M.R.P., Camargo A.A., Camargo L.B.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Racincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Al Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Al Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Al Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Al Lemos B.G.M., Lemos M.V.F., Lopes C.R., Machado J.A.,
Al Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marsukuma A.Y.,
Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Mardins G.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL080119; CAB45718.1; -.
EMBL; BC17449; AAH17449.1; --
Hypothetical protein.
SEQUENCE 387 **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21154917; PubMed=11230166; Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S. Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Lauber J., Ottenwaelder B., Obermaier B., Tampe J., Heubner D. Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D. Wambutt R., Korn B., Klein M., Poustka A., Tampe J., Heubner D. Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 42.4 kDa protein (PAI-1 mRNA-binding protein).
DKF2P564W2423.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PCI2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyrin biosynthesis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LUNG
                                                                                                                                                                                                                                                                                            MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 ADTENKE 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADTENKE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42426 MW; 8C47134D22C1CCFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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[00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glassl S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥,
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RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mhani A. Jr., Nobrega P.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Oliveira G.A.G., Pereira G.A.G., Pareira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Jr.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
"The genome sequence of the plant pathogen Xylella fastidiosa.";
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
"In genome sequence of the plant pathogen Xylella fastidiosa.";
RI Nature 406:151-159(2000).
DR EMBL; AE004001; AAF84605.1; -.
BR InterPro; IRR011440; TPR.
SQ SEQUENCE 389 AA; 44436 MW; 24597773D3632925 CRC64;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 988 LPPRGLL 994
Db 181 LPPRGLL 187

Search completed: April 22, 2003, 15:35:32

Job time: 72 secs
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